TEAM 2

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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/443,982*

DATE: 11/14/95
TIME: 16:09:01

INPUT SET: S7227.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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 1                                    SEQUENCE LISTING       ENTERED
 2
 3    (1)    General Information:
 4
 5         (i) APPLICANT: DIXIT, VISHVA M.
 6
 7        (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING
 8                  FAS-ASSOCIATED APOPTOSIS
 9
10       (iii) NUMBER OF SEQUENCES: 7
11
12        (iv) CORRESPONDENCE ADDRESS:
13              (A) ADDRESSEE: Morrison & Foerster
14              (B) STREET: 755 Page Mill Road
15             ·(C) CITY: Palo Alto
16              (D) STATE: CA
17              (E) COUNTRY: USA
18              (F) ZIP: 94304-1018
19
20         (v) COMPUTER READABLE FORM:
21              (A) MEDIUM TYPE: Floppy disk
22              (B) COMPUTER: IBM PC compatible
23              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24              (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26        (vi) CURRENT APPLICATION DATA:
27              (A) APPLICATION NUMBER: US 08/443,982
28              (B) FILING DATE: 18-MAY-1995
29              (C) CLASSIFICATION:
30
31      (viii) ATTORNEY/AGENT INFORMATION:
32              (A) NAME: Konski, Antoinette F.
33              (B) REGISTRATION NUMBER: 34,202
34              (C) REFERENCE/DOCKET NUMBER: 20344-21070.20
35
36        (ix) TELECOMMUNICATION INFORMATION:
37              (A) TELEPHONE: (415)813-5600
38              (B) TELEFAX: (415)494-0792
39              (C) TELEX: 706141 MRSNFOERS SFO
40
41
42    (2) INFORMATION FOR SEQ ID NO:1:
43
44         (i) SEQUENCE CHARACTERISTICS:
45              (A) LENGTH: 1642 base pairs
46              (B) TYPE: nucleic acid
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47              (C) STRANDEDNESS: single
48              (D) TOPOLOGY: linear
49
50       (ii) MOLECULE TYPE: cDNA
51
52
53       (ix) FEATURE:
54              (A) NAME/KEY: CDS
55              (B) LOCATION: 130..756
56
57       (ix) FEATURE:
58              (A) NAME/KEY: misc_feature
59              (B) LOCATION: 4..6
60              (D) OTHER INFORMATION: /note= "An in-frame stop codon 130
61     base pairs upstream of the initiator methionine"
62
63       (ix) FEATURE:
64              (A) NAME/KEY: polyA_signal
65              (B) LOCATION: 1636..1641
66              (D) OTHER INFORMATION: /note= "Potential poly(A)
67     adenylation signal"
68
69       (ix) FEATURE:
70              (A) NAME/KEY: misc_feature
71              (B) LOCATION: 198..753
72              (D) OTHER INFORMATION: /note= "Clone-15, 5' end of FADD"
73
74       (ix) FEATURE:
75              (A) NAME/KEY: misc_feature
76              (B) LOCATION: 249..753
77              (D) OTHER INFORMATION: /note= "Clone-8, 5' end of FADD"
78
79       (ix) FEATURE:
80              (A) NAME/KEY: misc_feature
81              (B) LOCATION: 177..658
82              (D) OTHER INFORMATION: /note= "Death Domain of FADD"
83
84       (ix) FEATURE:
85              (A) NAME/KEY: mutation
86              (B) LOCATION: replace(490..492, "")
87              (D) OTHER INFORMATION: /note= "For FADDmt, the sequence is
88     altered to either AAT or AAC and the corresponding codon from
89     Val to Asn"
90
91       (ix) FEATURE:
92              (A) NAME/KEY: misc_feature
93              (B) LOCATION: group(250..753, 232..753)
94              (D) OTHER INFORMATION: /note= "Corresponding amino acids
95     can comprise C-terminal polypeptide fragments of FADD"
96
97       (ix) FEATURE:
98              (A) NAME/KEY: misc_feature
99              (B) LOCATION: 253..753
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100          (D) OTHER INFORMATION: /note= "Corresponding amino acids
101    can comprise a polypeptide fragment of FADD designated NFD-2"
102
103       (ix) FEATURE:
104            (A) NAME/KEY: misc_feature
105            (B) LOCATION: 310..753
106            (D) OTHER INFORMATION: /note= "Corresponding amino acids
107    can comprise a polypeptide fragment of FADD designated NFD-3"
108
109       (ix) FEATURE:
110            (A) NAME/KEY: misc_feature
111            (B) LOCATION: 367..753
112            (D) OTHER INFORMATION: /note= "Corresponding amino acids
113    can comprise polypeptide fragment of FADD designated NFD-4"
114
115       (ix) FEATURE:
116            (A) NAME/KEY: misc_feature
117            (B) LOCATION: 131..504
118            (D) OTHER INFORMATION: /note= "Corresponding amino acids
119    can comprise an N-terminal half polypeptide fragment of FADD"
120
121       (ix) FEATURE:
122            (A) NAME/KEY: misc_feature
123            (B) LOCATION: 71..478
124            (D) OTHER INFORMATION: /note= "Corresponding amino acids
125    can comprise an N-terminal half polypeptide fragment of FADD
126    designated N-FADD"
127
128       (ix) FEATURE:
129            (A) NAME/KEY: misc_feature
130            (B) LOCATION: 133..501
131            (D) OTHER INFORMATION: /note= "Corresponding amino acids
132    can comprise an N-terminal half polypeptide fragment of FADD"
133
134
135       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
136
137    CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG      60
138
139    GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA     120
140
141    GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC        168
142              Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser
143                1           5                   10
144
145    AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG      216
146    Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly
147        15                  20                  25
148
149    CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC      264
150    Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu
151     30                  35                  40                  45
152
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153   TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG        312
154   Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu
155               50                      55                      60
156

157   CTC CTG CGC GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG        360
158   Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg
159               65                      70                      75
160

161   CGC GTC GAC GAC TTC GAG GCG GGG GCG GCG GCC GGG GCC GCG CCT GGG        408
162   Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly
163               80                      85                      90
164

165   GAA GAA GAC CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG        456
166   Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly
167             95                     100                     105
168

169   AAA GAT TGG AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG        504
170   Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys
171   110                     115                     120                 125
172

173   ATC GAC AGC ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG        552
174   Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val
175                    130                     135                     140
176

177   CGG GAG TCA CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA        600
178   Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr
179                    145                     150                     155
180

181   GTG GCC CAC CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG        648
182   Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val
183             160                     165                     170
184

185   GCT GAC CTG GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG        696
186   Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg
187         175                     180                     185
188

189   AGT GGG GCC ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC        744
190   Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser
191   190                     195                     200                 205
192

193   GAA GCG TCC TGA TGGGCCGCTG CTTTGCGCTG GTGGACCACA GGCATCTACA           796
194   Glu Ala Ser  *
195

196

197   CAGCCTGGAC TTTGGTTCTC TCCAGGAAGG TAGCCCAGCA CTGTGAAGAC CCAGCAGGAA       856
198

199   GCCAGGCTGA GTGAGCCACA GACCACCTGC TTCTGAACTC AAGCTGCGTT TATTAATGCC       916
200

201   TCTCCCGCAC CAGGCCGGGC TTGGGCCCTG CACAGATATT TCCATTTCTT CCTCACTATG       976
202

203   ACACTGAGCA AGATCTTGTC TCCACTAAAT GAGCTCCTGC GGGAGTAGTT GGAAAGTTGG      1036
204

205   AACCGTGTCC AGCACAGAAG GAATCTGTGC AGATGAGCAG TCACACTGTT ACTCCACAGC      1096
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206
207   GGAGGAGACC AGCTCAGAGG CCCAGGAATC GGAGCGAAGC AGAGAGGTGG AGAACTGGGA    1156
208
209   TTTGAACCCC CGCCATCCTT CACCAGAGCC CATGCTCAAC CACTGTGGCG TTCTGCTGCC    1216
210
211   CCTGCAGTTG GCAGAAAGGA TGTTTTGTCC CATTTCCTTG GAGGCCACCG GGACAGACCT    1276
212
213   GGACACTAGG GTCAGGCGGG GTGCTGTGGT GGGGAGAGGC ATGGCTGGGG TGGGGGTGGG    1336
214
215   GAGACCTGGT TGGCCGTGGT CCAGCTCTTG GCCCCTGTGT GAGTTGAGTC TCCTCTCTGA    1396
216
217   GACTGCTAAG TAGGGGCAGT GATGGTTGCC AGGACGAATT GAGATAATAT CTGTGAGGTG    1456
218
219   CTGATGAGTG ATTGACACAC AGCACTCTCT AAATCTTCCT TGTGAGGATT ATGGGTCCTG    1516
220
221   CAATTCTACA GTTTCTTACT GTTTTGTATC AAAATCACTA TCTTTCTGAT AACAGAATTG    1576
222
223   CCAAGGCAGC GGGATCTCGT ATCTTTAAAA AGCAGTCCTC TTATTCCTAA GGTAATCCTA    1636
224
225   TTAAAA                                                               1642
226
227
228   (2) INFORMATION FOR SEQ ID NO:2:
229
230           (i) SEQUENCE CHARACTERISTICS:
231               (A) LENGTH:  208 amino acids
232               (B) TYPE: amino acid
233               (D) TOPOLOGY: linear
234
235       (ii) MOLECULE TYPE: protein
236
237       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
238
239   Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
240    1               5              10               15
241
242   Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
243           20               25               30
244
245   Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
246           35               40               45
247
248   Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
249       50               55               60
250
251   Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
252    65               70               75               80
253
254   Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
255                85               90               95
256
257   Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
258               100              105              110
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/443,982*

INPUT SET: S7227.raw

Line	Error	Original Text
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